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1600

RAW SEQUENCE LISTING

DATE: 02/11/2003

PATENT APPLICATION: US/08/599,974E

TIME: 10:56:27

Input Set : A:\EP.txt

Output Set: N:\CRF4\02112003\H599974E.raw

3 <110> APPLICANT: The Rockefeller University
 4 Friedman, Jeffrey M.
 5 Lee, Gwo-Hwa
 6 Proenca, Ricardo
 8 <120> TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC ACIDS ENCODING THE
 RECEPTOR, AND USES
 9 THEREOF
 11 <130> FILE REFERENCE: 600-1-162CP1
 13 <140> CURRENT APPLICATION NUMBER: 08/599,974E
 14 <141> CURRENT FILING DATE: 1996-02-14
 16 <150> PRIOR APPLICATION NUMBER: US 09/586,594
 17 <151> PRIOR FILING DATE: 1996-01-16
 19 <160> NUMBER OF SEQ ID NOS: 97
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2529
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Mus musculus
 28 <400> SEQUENCE: 1

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33	aatgagcaag	gtcaaaactg	ctctgcactc	acagacaaca	ctgaaggga	gacactggct	180
35	tcagtagtga	aggcttcagt	tttcgccag	ctaggtgtaa	actgggacat	agagtgtctg	240
37	atgaaagggg	acttgacatt	attcatctgt	catatggagc	cattacctaa	gaacccttc	300
39	aagaattatg	actctaaggt	ccatctttta	tatgatctgc	ctgaagtcac	agatgattcg	360
41	cctctgcccc	cactgaaaga	cagctttcag	actgtccaat	gcaactgcag	tcttcgggga	420
43	tgtgaatgtc	atgtgcgggt	acccagagcc	aaactcaact	acgctcttct	gatgtatttg	480
45	gaaatcacat	ctgccgggtg	gagttttcag	tcacctctga	tgtcactgca	gcccattgct	540
47	gttgtgaaac	ccgatccacc	cttaggtttg	catatggaag	tcacagatga	tggtaattta	600
49	aagatttctt	gggacagcca	aacaatggca	ccatttcgcg	ttcaatatca	ggtgaaatat	660
51	ttagagaatt	ctacaattgt	aagagaggct	gctgaaattg	tctcagctac	atctctgctg	720
53	gtagacagt	tgcttcctgg	atcttcatat	gaggtccagg	tgaggagcaa	gagactggat	780
55	ggttcaggag	tctggagtga	ctggagttca	cctcaagtct	ttaccacaca	agatgtttgt	840
57	tattttccac	ccaaaattct	gactagtgtt	ggatcgaatg	cttcttttca	ttgcatctac	900
59	aaaaacgaaa	accagattat	ctcctcaaaa	cagatagttt	ggtggaggga	tctagctgag	960
61	aaaatccctg	agatacagta	cagcattgtg	agtgaccgag	ttagcaaagt	taccttctcc	1020
63	aacctgaaag	ccaccagacc	tcgagggaag	ttacctatg	acgcagtgtg	ctgctgcaat	1080
65	gagcaggcgt	gccatcaccg	ctatgctgaa	ttatacgtga	tcgatgtcaa	tatcaatata	1140
67	tcattgtgaa	ctgacgggta	cttaactaaa	atgacttgca	gatggtcacc	cagcacaatc	1200
69	caatcactag	tgggaagcac	tgtgcagctg	aggtatcaca	ggcgagacct	gtattgtcct	1260
71	gatagtccat	ctattcatcc	tacgtctgag	cccaaaaact	gcgtcttaca	gagagacggc	1320
73	ttttatgaat	gtgtttttcca	gccaatcttt	ctattatctg	gctatacaat	gtggatcagg	1380
75	atcaaccatt	cttttaggttc	acttgactcg	ccaccaacgt	gtgtccttcc	tgactccgta	1440
77	gtaaaaccac	tacctccatc	taacgtaaaa	gcagagatta	ctgtaaacac	tggattattg	1500

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79 aaagtatctt gggaaaagcc agtctttccg gagaataacc ttcaattcca gattcgatat 1560
81 ggcttaagtg gaaaagaaat acaatggaag acacatgagg tattcgatgc aaagtcaaag 1620
83 tctgccagcc tgctggtgtc agacctctgt gcagtctatg tgggccaggt tcgctgccgg 1680
85 cggttggatg gactaggata ttggagtaat tggagcagtc cagcctatac gcttgatcag 1740
87 gatgtaaaag ttcctatgag agggcctgaa ttttggagaa aaatggatgg ggacgttact 1800
89 aaaaaggaga gaaatgtcac cttgctttgg aagcccctga cgaaaaatga ctactgtgt 1860
91 agtgtgagga ggtacgtggt gaagcatcgt actgccaca atgggacgtg gtcagaagat 1920
93 gtgggaaatc ggaccaatct cactttcctg tggacagaac cagcgcacac tgttacagtt 1980
95 ctggctgtca attccctcgg cgcttcctt gtgaatttta accttacctt ctcatggccc 2040
97 atgagtaaag tgagtgtgtg ggagtcactc agtgcttata ccctgagcag cagctgtgtc 2100
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103 ttttatatcc acgataatct tattcccatc gagaaatata agtttagtct ttaccagta 2280
105 tttatggaag gagttgaaa accaaagata attaatggtt tcaccaaaga tgctatcgac 2340
107 aagcagcaga atgacgcagg gctgtatgtc attgtacca taattatttc ctctgtgtc 2400
109 ctactgtctg gaacactgtt aatttcacac cagagaatga aaaagttgtt ttgggacgat 2460
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116 <210> SEQ ID NO: 2

117 <211> LENGTH: 842

118 <212> TYPE: PRT

119 <213> ORGANISM: Mus musculus

121 <220> FEATURE:

122 <221> NAME/KEY: MISC_FEATURE

123 <222> LOCATION: (29)..(29)

124 <223> OTHER INFORMATION: X can be any amino acid

127 <400> SEQUENCE: 2

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130 1 5 10 15

W--> 133 Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro

134 20 25 30

137 Asn Ser Ala Arg Gly Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser

138 35 40 45

141 Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys

142 50 55 60

145 Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp

146 65 70 75 80

149 Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Pro

150 85 90 95

153 Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp

154 100 105 110

157 Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro Leu Lys Asp Ser

158 115 120 125

161 Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His

162 130 135 140

165 Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu Leu Met Tyr Leu

166 145 150 155 160

169 Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu

170 165 170 175

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173 Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
174      180      185      190
177 Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr
178      195      200      205
181 Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser
182      210      215      220
185 Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu
186 225      230      235      240
189 Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser
190      245      250      255
193 Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln
194      260      265      270
197 Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr
198      275      280      285
201 Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn
202      290      295      300
205 Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu
206 305      310      315      320
209 Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys
210      325      330      335
213 Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr
214      340      345      350
217 Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr
218      355      360      365
221 Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr
222      370      375      380
225 Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile
226 385      390      395      400
229 Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser
230      405      410      415
233 Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys
234      420      425      430
237 Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro
238      435      440      445
241 Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser
242      450      455      460
245 Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val
246 465      470      475      480
249 Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu Ile Thr Val Asn
250      485      490      495
253 Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val Phe Pro Glu Asn
254      500      505      510
257 Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Ile Gln
258      515      520      525
261 Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys Ser Ala Ser Leu
262      530      535      540
265 Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln Val Arg Cys Arg
266 545      550      555      560
269 Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Ser Pro Ala Tyr

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270          565          570          575
273 Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly Pro Glu Phe Trp
274          580          585          590
277 Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg Asn Val Thr Leu
278          595          600          605
281 Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg
282          610          615          620
285 Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp
286 625          630          635          640
289 Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His
290          645          650          655
293 Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn
294          660          665          670
297 Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu
298          675          680          685
301 Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp
302          690          695          700
305 Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp
306 705          710          715          720
309 Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser
310          725          730          735
313 Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys
314          740          745          750
317 Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro
318          755          760          765
321 Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn
322          770          775          780
325 Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile Ser Ser Cys Val
326 785          790          795          800
329 Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu
330          805          810          815
333 Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly
334          820          825          830
337 Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu
338          835          840
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342 <211> LENGTH: 2848
343 <212> TYPE: DNA
344 <213> ORGANISM: Mus musculus
346 <220> FEATURE:
347 <221> NAME/KEY: misc_feature
348 <222> LOCATION: (44)..(44)
349 <223> OTHER INFORMATION: N can be A, C, T or G
352 <220> FEATURE:
353 <221> NAME/KEY: misc_feature
354 <222> LOCATION: (67)..(67)
355 <223> OTHER INFORMATION: N can be A, C, T or G
358 <220> FEATURE:
359 <221> NAME/KEY: misc_feature

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360 <222> LOCATION: (234)..(234) ✓
361 <223> OTHER INFORMATION: N can be A, C, T or G
364 <220> FEATURE:
365 <221> NAME/KEY: misc_feature
366 <222> LOCATION: (483)..(483) ✓
367 <223> OTHER INFORMATION: N can be A, C, T or G
370 <220> FEATURE:
371 <221> NAME/KEY: misc_feature
372 <222> LOCATION: (527)..(527) ✓
373 <223> OTHER INFORMATION: N can be A, C, T or G
376 <220> FEATURE:
377 <221> NAME/KEY: misc_feature
378 <222> LOCATION: (564)..(564) ✓
379 <223> OTHER INFORMATION: N can be A, C, T or G
382 <220> FEATURE:
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384 <222> LOCATION: (1237)..(1237) ✓
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397 <223> OTHER INFORMATION: N can be A, C, T or G
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402 <222> LOCATION: (2179)..(2179) ✓
403 <223> OTHER INFORMATION: N can be A, C, T or G
406 <220> FEATURE:
407 <221> NAME/KEY: misc_feature
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409 <223> OTHER INFORMATION: N can be A, C, T or G
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413 <221> NAME/KEY: misc_feature
414 <222> LOCATION: (2183)..(2183) ✓
415 <223> OTHER INFORMATION: N can be A, C, T or G
418 <220> FEATURE:
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420 <222> LOCATION: (2219)..(2219) ✓
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425 <221> NAME/KEY: misc_feature
426 <222> LOCATION: (2576)..(2576) ✓
427 <223> OTHER INFORMATION: N can be A, C, T or G
430 <220> FEATURE:
431 <221> NAME/KEY: misc_feature
432 <222> LOCATION: (2610)..(2610)

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 29
Seq#:3; N Pos. 44, 67, 234, 483, 527, 564, 1237, 1335, 2038, 2179, 2182, 2183, 2219
Seq#:3; N Pos. 2576, 2610
Seq#:4; Xaa Pos. 79
Seq#:5; N Pos. 160, 258
Seq#:6; Xaa Pos. 14, 19, 25, 58, 67, 68, 84, 86
Seq#:35; N Pos. 5
Seq#:39; N Pos. 55, 62, 72, 143
Seq#:40; N Pos. 83, 101, 181
Seq#:41; N Pos. 193
Seq#:57; Xaa Pos. 29
Seq#:58; Xaa Pos. 29
Seq#:59; Xaa Pos. 29
Seq#:60; Xaa Pos. 79
Seq#:61; Xaa Pos. 14, 19, 25, 58, 67, 68, 84, 86
Seq#:62; Xaa Pos. 79
Seq#:63; Xaa Pos. 14, 19, 25, 58, 67, 68, 84, 86

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 8